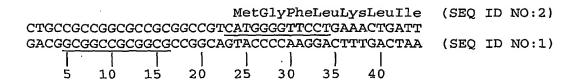
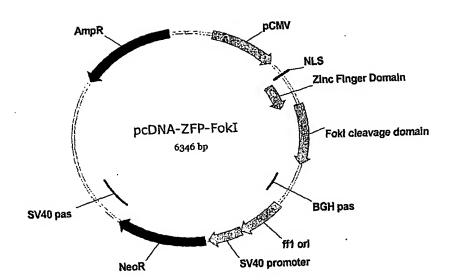
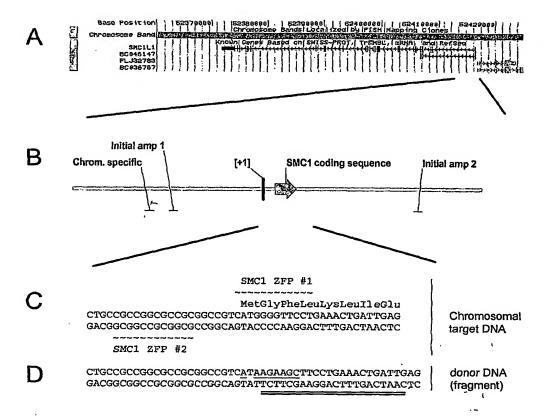
WO 2005/084190

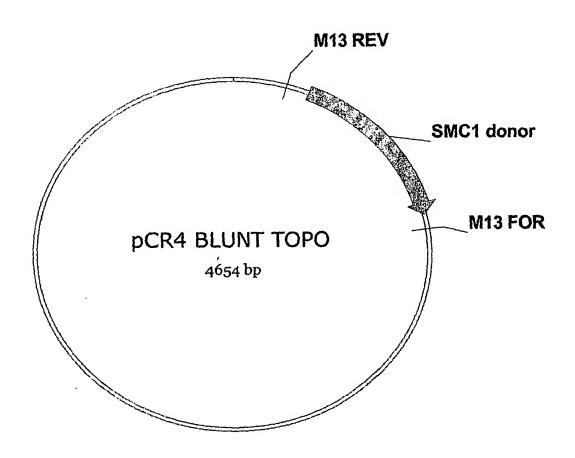
1/45

PCT/US2005/003245









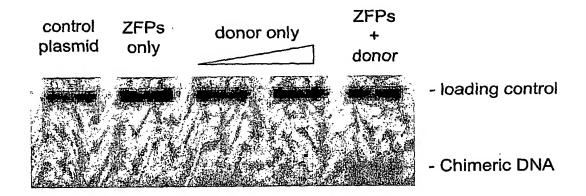
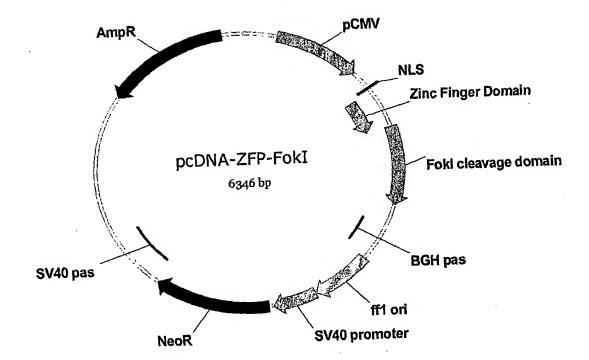


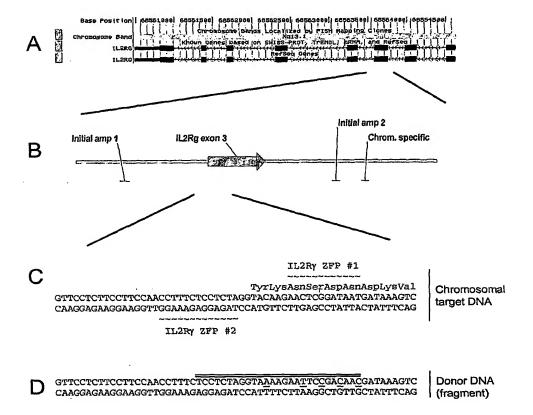
FIGURE 6

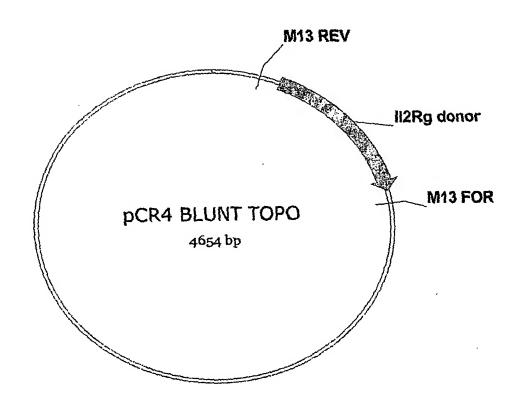
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GGTCTCCCCGCCTCCTTGAACCTCAAGAACTGCTCTGACTCCGCCCAGC	100
AACAACTCCTCCGGGGATCTGGTCCGCAGGAGCAAGTGTTTGTT	150
ATGCAACAAGAAAAGGGGGGGGGGGCACCACGCCAGTCGTCAGCTCGCTC	200
CTCGTATACGCAACATCAGTCCCCGCCCCTGGTCCCACTCCTGCCGGAAG	250
GCGAAGATCCCGTTAGGCCTGGACGTATTCTCGCGACATTTGCCGGTCGC	300
CCGGCTTGCACTGCGGCGTTTCCCGCGCGGGCTACCTCAGTTCTCGGGCG	350
TACGGCGCGCCTGTCCTACTGCTGCCGGCGCCGCCGCCGTCATaagaag	400
<u>CTTCCTGAAACTGATTGAAGGGCGAATTCGCGGCCGCTAAATTCAATTCG</u>	450
CCCTATAGTGAGT	

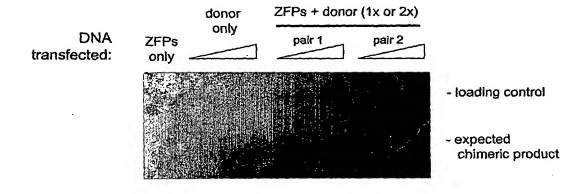
(SEQ ID NO: 6)

				TyrLy	/sAsnS	SerAsı	AsnAs	pLys	7al	(SEQ	ID
NO:8)											
CTTCCA	ACCTTT	CTCC	CTAG	TACA	AGAAC'	rcgga1	AATG	YAAAT	STCC		
GAAGGT'	TGGAAZ	AGAGG	AGATC	ATGT	CTTG	AGCCTZ	TTACT)TTTA	CAGG	(SEQ	ID
NO:7)											
ì	- 1	1	- 1			1			4		
έ	1 0	15	2Ò	25	3 กั	35	40	45	50		









TAGTCCTGCAGGTTTAAACGAATTCGCCCTTTCCTCTAGGTAaAAGAALT	50
CCGACAACGATAAAGTCCAGAAGTGCAGCCACTATCTATTCCCTGAAGAA	100
ATCACTTCTGGCTGTCAGTTGCAAAAAAAGGAGATCCACCTCTACCAAAC	150
ATTTGTTGTTCAGCTCCAGGACCCACGGGAACCCAGGAGACAGGCCACAC	200
AGATGCTAAAACTGCAGAATCTGGGTAATTTGGAAAGAAA	250
ACCAGGGATACTGTGGGACATTGGAGTCTACAGAGTAGTGTTCTTTTATC	300
ATAAGGGTACATGGGCAGAAAAGAGGGGGTAGGGGATCATGATGGGAAGG	350
GAGGAGGTATTAGGGGCACTACCTTCAGGATCCTGACTTGTCTAGGCCAG	400
GGGAATGACCACATATGCACACATATCTCCAGTGATCCCCTGGGCTCCAG	450
AGAACCTAACACTTCACAAACTGAGTGAATCCCAGCTAGAACTGAACTGG	500
AACAACAGATTCTTGAACCACTGTTTGGAGCACTTGGTGCAGTACCGGAC	550
TAAGGGCGAATTCGCGGCCGCTAAATTCAATTCGCCCTATAGTGAGTCGT	600
A DULA CA A DULCA CUCCACCULCAUTU	

(SEQ ID NO:12)

TACTGATGGTATGGGGCCAAGAGATATATCTTAGAGGGAGG	50
TTGAAGTCCAACTCCTAAGCCAGTGCCAGAAGAGCCAAGGACAGGTACGG	100
CTGTCATCACTTAGACCTCACCCTGTGGAGCCACACCCTAGGGTTGGCCA	150
ATCTACTCCCAGGAGCAGGAGGCAGGAGCCAGGGCTGGGCATAAAAGT	200
CAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGACACAACTGTGTTC	250
ACTAGCAACCTCAAACAGACACCATGGTGCATCTGACTCCTG <u>A</u> GGAGAAG	300
TCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGG	350
TGAGGCCCTGGGCAGGTTGGTATCAAGGTTACAAGACAGGTTTAAGGAGA	400
CCAATAGAAACTGGGCATGTGGAGACAGAGAAGACTCTTGGGTTTCTGAT	450
AGGCACTGACTCTCTGCCTATTGGTCTATTTTCCCACCCTTAGGCTGC	500
TGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGATCTG	550
TCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAA	600
GAAAGTGCTCGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCA	650
AGGGCACCTTTGCCACACTGAGTGAGCTGCACTGTGACAAGCTGCACGTG	700

(SEQ ID NO:13)

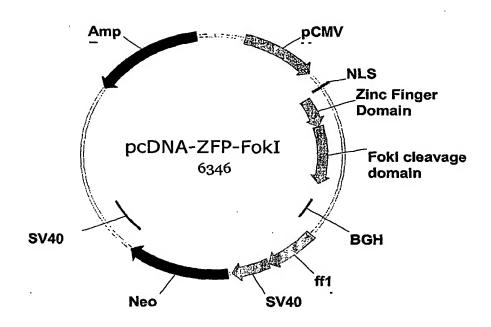
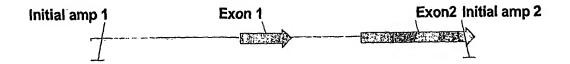
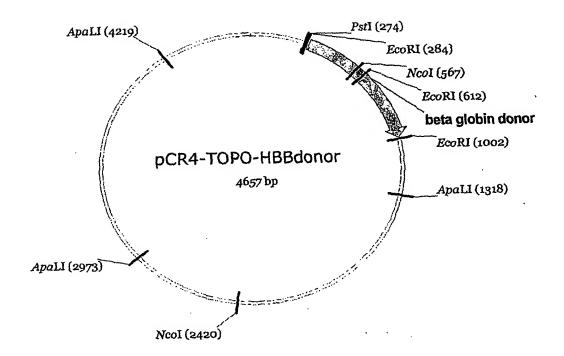
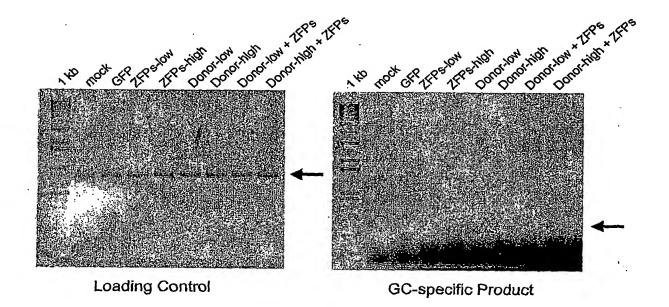


FIGURE 15



Beta globin human genomic TARGET 700 bp





TGCTTACCAAGCTGTGATTCCAAATATTACGTAAATACACTTGCAAAGGA	.50
GGATGTTTTTAGTAGCAATTTGTACTGATGGTATGGGGCCCAAGAGATATA	100
TCTTAGAGGGAGGGCTGAGGGTTTGAAGTCCAACTCCTAAGCCAGTGCCA	150
GAAGAGCCAAGGACAGGTACGGCTGTCATCACTTAGACCTCACCCTGTGG	200
AGCCACACCCTAGGGTTGGCCAATCTACTCCCAGGAGCAGGGAGGG	250
AGCCAGGGCTGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACATT	300
TGCTTCTGACACAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGT	350
GCATCTGACTCCTGAGGAGAAGTCTG <u>gCGTTAgTGCCCgaattccgAtcG</u>	400
TCAACCaC	

(SEQ ID NO:14)

5-8
CACGTTTCGTGTTCGGAGCCGCTTTAACCCACTCTGTGGAAG
GTGCAAAGCACAAGCCTCGGCGAAATTGGGTGAGACACCTTC
5-10

(SEQ ID NO:15)

	Mapkkkrkvg					
						DICGRKFAAR
						IARNSTQDRI
181	LEMKVMEFFM	KVYGYRGKHL	GGSRKPDGAI	YTVGSPIDYG	VIVDTKAYSG	GYNLPIGQAD
					FKGNYKAQLT	RLNHITNCNG
301	AVLSVEELLI	GGEMIKAGTL	TLEEVRRKFN	NGEINF		

(SEQ ID NO:16)

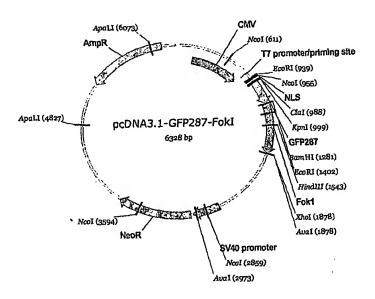
1	MAPKKKRKVG	IHGVPAAMAE	RPFQCRICMR	NESRSDSLSR	HIRTHTGEKP	FACDICGRKF
61	A DSSNRKT HT	KIHTGGGGSQ	KPFQCRICMR	NFSRSDSLSV	HIRTHTGEKP	FACDICGRKF
121	ADRSNRITHT	KIHLRQKDAA	RGSQLVKSEL	EEKKSELRHK	LKYVPHEYIE	LIEIARNSTQ
181	DRILEMKVME	FFMKVYGYRG	KHLGGSRKPD	GAIYTVGSPI	DYGVIVDTKA	YSGGYNLPIG
241	QADEMQRYVE	ENQTRNKHIN	PNEWWKVYPS	SVTEFKFLFV	SGHFKGNYKA	QLTRLNHITN
	CNGAVLSVEE					

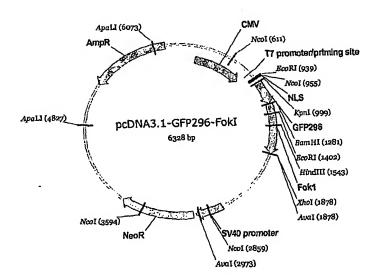
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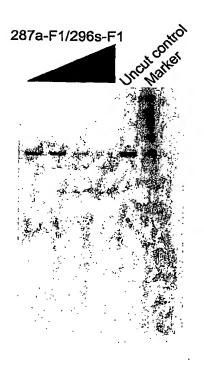
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AAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTA
AACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTG
ACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACC
ACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACTGAAGCACCACGAC
TTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGAC
GACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGC
ATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGCAACATCCTGGGGCACAAGCTGGAG
TACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAG
GTGAACTTCAAGATCCGCCACAACATCGAGGACGCAGCGTGCAGCTCGCCGACCACTAC
CAGCAGAACACCCCCATCGGCGACGCCCCGTGCTGCTCCCGACAACCACTACCTGAGC
ACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAG
GTTCGTGACCGCCGCGGGATCACTCTCCGGCATGACGACGACCACTACCTGAGC
GACTCTAGATCATAATC

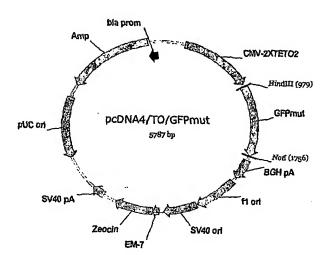
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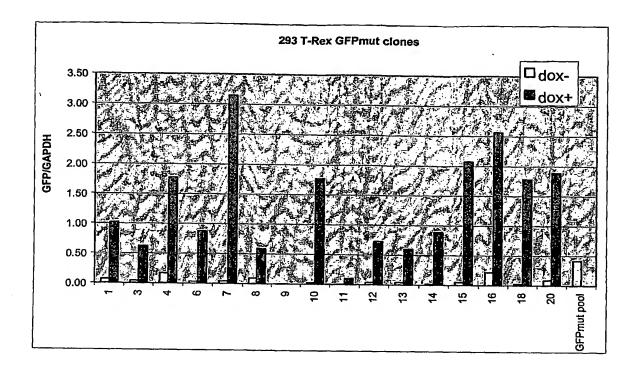
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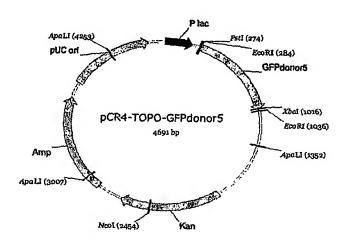




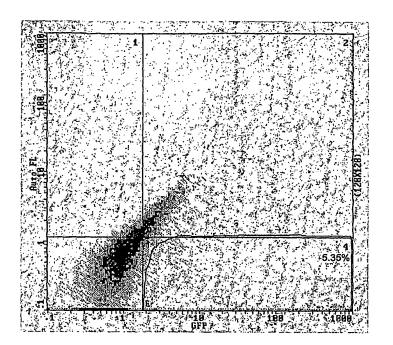


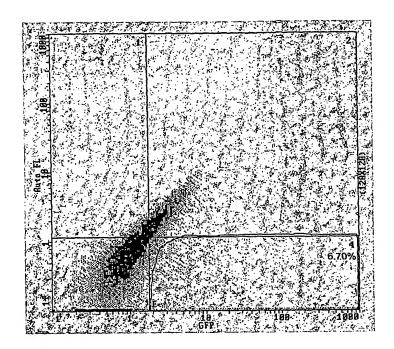






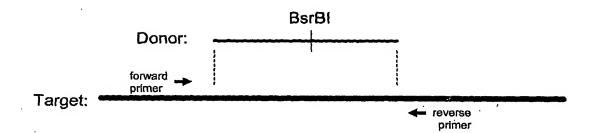
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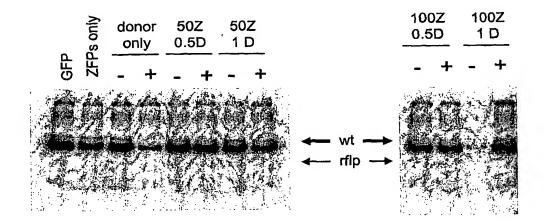


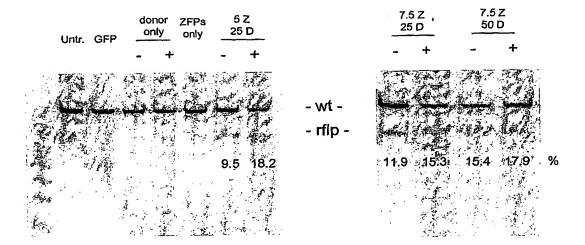


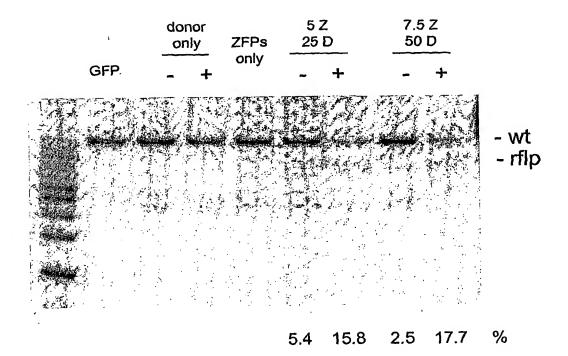
GGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAAC GGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACC CTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACC CTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACGTGAAGCAGCACGACTTC TTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGAC GGCAACTACAAGACCCGCGCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATC GAGCTGAAGGGCATCGACTTCAAGGAGGACGCAACATCCTGGGGCACAAGCTGGAGTAC AACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCCATCAAGGTG AACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAG CAGAACACCCCCATCGGCGACGGCCCCGTGCTGCCCGACAACCACTACCTGAGCACC CAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTC GTGACCGCCGCGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAAGCGGCCGCTCG AGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGC CATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTG TCCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTC TGGGGGTGGGGTGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATG $\tt CTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCTCTAGGG$ GGTATCCCCACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGTGTGGTGGTTACGCGCA GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCT TTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGT TCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCAC GTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCT TTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTT TTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAAC AAAAATTTAACGCGAATTAATTCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCC AGGCTCCCCAGCAGGCAGAAGTATGCA

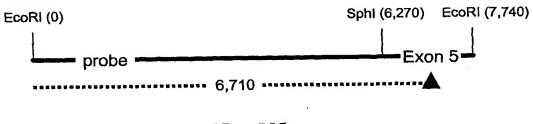
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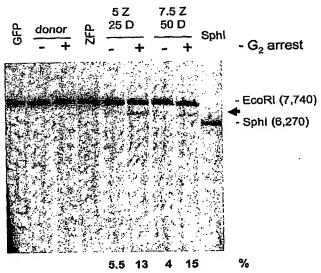


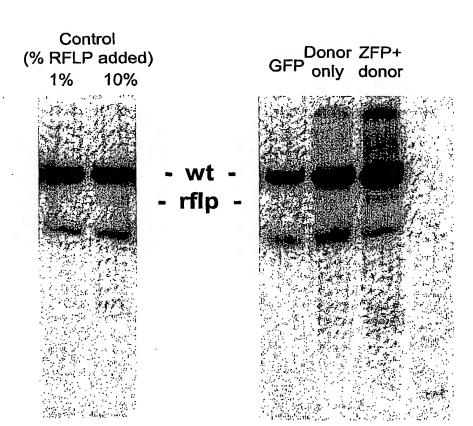












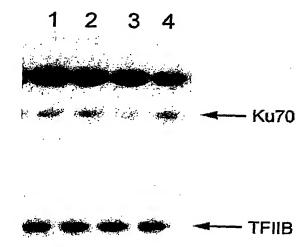


FIGURE 40

sca-29b:

MAERPFQCRICMRNFSQSGDLTRHIRTHTGEKPFACDICGRKFATSANLSRHTK IHTGGGGSQKPFQCRICMRNFSDRSALSRHIRTHTGEKPFACDICGRKFAQSGHLSRHTKIH (SEQ ID NO:22)

sca-36a:

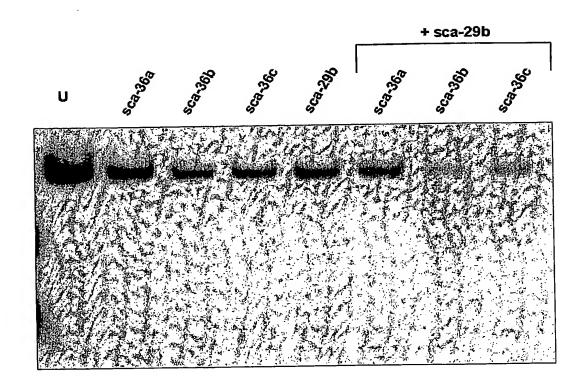
MAERPFQCRICMRNFS<u>RSQTRKT</u>HIRTHTGEKPFACDICGRKFA<u>QKRNRTK</u>HT KIHTGSQKPFQCRICMRNFS<u>DRSALSR</u>HIRTHTGEKPFACDICGRKFA<u>QSGNLA</u> <u>R</u>HTKIH (SEQ ID NO:23)

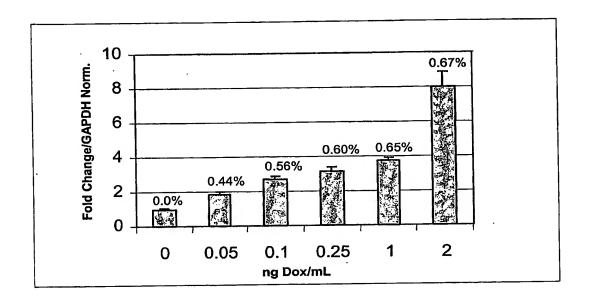
sca-36b:

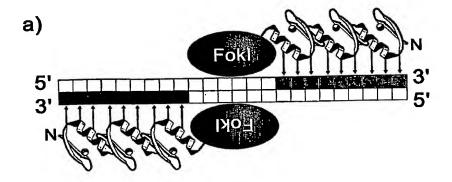
MAERPFQCRICMRNFS<u>TSGSLSR</u>HIRTHTGEKPFACDICGRKFA<u>DRSDLSR</u>HTK IHTGGGGSQKPFQCRICMRNFS<u>DRSALSR</u>HIRTHTGEKPFACDICGRKFA<u>QSG</u> <u>NLAR</u>HTKIH (SEQ ID NO:24)

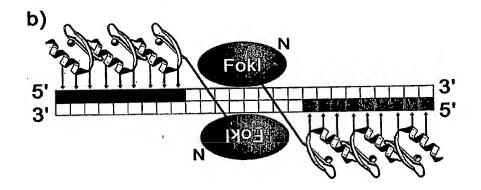
sca-36c:

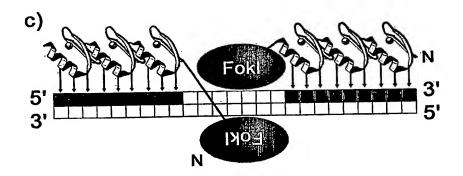
MAERPFQCRICMRNFS<u>TSSSLSR</u>HIRTHTGEKPFACDICGRKFA<u>DRSDLSR</u>HTK IHTGGGGSQKPFQCRICMRNFS<u>DRSALSR</u>HIRTHTGEKPFACDICGRKFA<u>QSG</u> NLARHTKIH (SEQ ID NO:25)

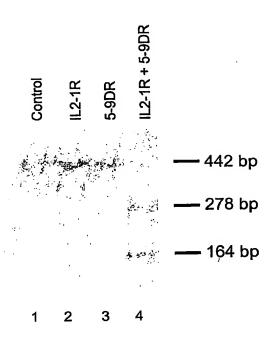






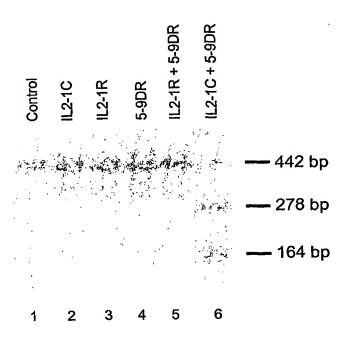






59D
-tAAAGCGGCTCCGaaccacATTATCCGAGTTc-aTTTCGCCGAGGCttggtgTAATAGGCTCAAgIL2-1

(SEQ ID NO: 211)



59D IL2-1
-tAAAGCGGCTCCGaaccacAACTCGGATAATg-aTTTCGCCGAGGCttggtgTTGAGCCTATTAc-

(SEQ ID NO: 212)

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